```
cgctctagcc cggtgggaag ctttcatcca gaaca atg aat ttc ata aag gac          53
                                          Met Asn Phe Ile Lys Asp
                                          1                     5


aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa        101
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln
            10                  15                  20


atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta        149
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
            25                  30                  35


aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc        197
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile
        40                  45                  50


att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt        245
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu
    55                  60                  65                  70


aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga        293
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly
                75                  80                  85


caa agt ctt ttt cat cag aca tca gaa gga gac ttg gac gat ttg gct        341
Gln Ser Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp Asp Leu Ala
                90                  95                  100


cag gat tta aag gac ttg tac cat acc cca tct ttt ctg aac ttt tat        389
Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu Asn Phe Tyr
            105                 110                 115


ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa agc acc ttc        437
Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe Asn Leu Lys Ser Thr Phe
    120                 125                 130


aca gaa cct gtc ctg tgg agg aag gac caa cac cat cac cgc gtg gag        485
Thr Glu Pro Val Leu Trp Arg Lys Asp Gln His His His Arg Val Glu
135                 140                 145                 150


cag ctg acc ctg aat ggc ctc ctg cag gct ctt cag agc ccc tgc atc       533
Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala Leu Gln Ser Pro Cys Ile
                155                 160                 165


att gaa ggg gaa tct ggc aaa ggc aag tcc act ctg ctg cag cgc att        581
Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser Thr Leu Leu Gln Arg Ile
                170                 175                 180


gcc atg ctc tgg ggc tcc gga aag tgc aag gct ctg acc aag ttc aaa        629
Ala Met Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr Lys Phe Lys
            185                 190                 195


ttc gtc ttc ttc ctc cgt ctc agc agg gcc cag ggt gga ctt ttt gaa       677
Phe Val Phe Phe Leu Arg Leu Ser Arg Ala Gln Gly Gly Leu Phe Glu
    200                 205                 210
```

Fig. 1A

```
acc ctc tgt gat caa ctc ctg gat ata cct ggc aca atc agg aag cag      725
Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro Gly Thr Ile Arg Lys Gln
215                 220             225                 230

aca ttc atg gcc atg ctg ctg aag ctg cgg cag agg gtt ctt ttc ctt      773
Thr Phe Met Ala Met Leu Leu Lys Leu Arg Gln Arg Val Leu Phe Leu
                235             240             245

ctt gat ggc tac aat gaa ttc aag ccc cag aac tgc cca gaa atc gaa      821
Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln Asn Cys Pro Glu Ile Glu
                250             255             260

gcc ctg ata aag gaa aac cac cgc ttc aag aac atg gtc atc gtc acc      869
Ala Leu Ile Lys Glu Asn His Arg Phe Lys Asn Met Val Ile Val Thr
                265             270             275

act acc act gag tgc ctg agg cac ata cgg cag ttt ggt gcc ctg act      917
Thr Thr Thr Glu Cys Leu Arg His Ile Arg Gln Phe Gly Ala Leu Thr
    280             285             290

gct gag gtg ggg gat atg aca gaa gac agc gcc cag gct ctc atc cga      965
Ala Glu Val Gly Asp Met Thr Glu Asp Ser Ala Gln Ala Leu Ile Arg
295             300             305             310

gaa gtg ctg atc aag gag ctt gct gaa ggc ttg ttg ctc caa att cag     1013
Glu Val Leu Ile Lys Glu Leu Ala Glu Gly Leu Leu Leu Gln Ile Gln
                315             320             325

aaa tcc agg tgc ttg agg aat ctc atg aag acc cct ctc ttt gtg gtc     1061
Lys Ser Arg Cys Leu Arg Asn Leu Met Lys Thr Pro Leu Phe Val Val
                330             335             340

atc act tgt gca atc cag atg ggt gaa agt gag ttc cac tct cac aca     1109
Ile Thr Cys Ala Ile Gln Met Gly Glu Ser Glu Phe His Ser His Thr
                345             350             355

caa aca acg ctg ttc cat acc ttc tat gat ctg ttg ata cag aaa aac     1157
Gln Thr Thr Leu Phe His Thr Phe Tyr Asp Leu Leu Ile Gln Lys Asn
    360             365             370

aaa cac aaa cat aaa ggt gtg gct gca agt gac ttc att cgg agc ctg     1205
Lys His Lys His Lys Gly Val Ala Ala Ser Asp Phe Ile Arg Ser Leu
375             380             385             390

gac cac tgt gga gac cta gct ctg gag ggt gtg ttc tcc cac aag ttt     1253
Asp His Cys Gly Asp Leu Ala Leu Glu Gly Val Phe Ser His Lys Phe
                395             400             405

gat ttc gaa ctg cag gat gtg tcc agc gtg aat gag gat gtc ctg ctg     1301
Asp Phe Glu Leu Gln Asp Val Ser Ser Val Asn Glu Asp Val Leu Leu
            410             415             420

aca act ggg ctc ctc tgt aaa tat aca gct caa agg ttc aag cca aag     1349
Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala Gln Arg Phe Lys Pro Lys
            425             430             435
```

Fig. 1B

```
tat aaa ttc ttt cac aag tca ttc cag gag tac aca gca gga cga aga      1397
Tyr Lys Phe Phe His Lys Ser Phe Gln Glu Tyr Thr Ala Gly Arg Arg
    440             445                 450

ctc agc agt tta ttg acg tct cat gag cca gag gag gtg acc aag ggg      1445
Leu Ser Ser Leu Leu Thr Ser His Glu Pro Glu Glu Val Thr Lys Gly
455             460                 465                 470

aat ggt tac ttg cag aaa atg gtt tcc att tcg gac att aca tcc act      1493
Asn Gly Tyr Leu Gln Lys Met Val Ser Ile Ser Asp Ile Thr Ser Thr
            475                 480                 485

tat agc agc ctg ctc cgg tac acc tgt ggg tca tct gtg gaa gcc acc      1541
Tyr Ser Ser Leu Leu Arg Tyr Thr Cys Gly Ser Ser Val Glu Ala Thr
            490                 495                 500

agg gct gtt atg aag cac ctc gca gca gtg tat caa cac ggc tgc ctt      1589
Arg Ala Val Met Lys His Leu Ala Ala Val Tyr Gln His Gly Cys Leu
            505                 510                 515

ctc gga ctt tcc atc gcc aag agg cct ctc tgg aga cag gaa tct ttg      1637
Leu Gly Leu Ser Ile Ala Lys Arg Pro Leu Trp Arg Gln Glu Ser Leu
            520                 525                 530

caa agt gtg aaa aac acc act gag caa gaa att ctg aaa gcc ata aac      1685
Gln Ser Val Lys Asn Thr Thr Glu Gln Glu Ile Leu Lys Ala Ile Asn
535             540                 545                 550

atc aat tcc ttt gta gag tgt ggc atc cat tta tat caa gag agt aca      1733
Ile Asn Ser Phe Val Glu Cys Gly Ile His Leu Tyr Gln Glu Ser Thr
            555                 560                 565

tcc aaa tca gcc ctg agc caa gaa ttt gaa gct ttc ttt caa ggt aaa      1781
Ser Lys Ser Ala Leu Ser Gln Glu Phe Glu Ala Phe Phe Gln Gly Lys
            570                 575                 580

agc tta tat atc aac tca ggg aac atc ccc gat tac tta ttt gac ttc      1829
Ser Leu Tyr Ile Asn Ser Gly Asn Ile Pro Asp Tyr Leu Phe Asp Phe
            585                 590                 595

ttt gaa cat ttg ccc aat tgt gca agt gct ctg gac ttc att aaa ctg      1877
Phe Glu His Leu Pro Asn Cys Ala Ser Ala Leu Asp Phe Ile Lys Leu
    600                 605                 610

gac ttt tat ggg gga gct atg gct tca tgg gaa aag gct gca gaa gac      1925
Asp Phe Tyr Gly Gly Ala Met Ala Ser Trp Glu Lys Ala Ala Glu Asp
615                 620                 625                 630

aca ggt gga atc cac atg gaa gag gcc cca gaa acc tac att ccc agc      1973
Thr Gly Gly Ile His Met Glu Glu Ala Pro Glu Thr Tyr Ile Pro Ser
                635                 640                 645

agg gct gta tct ttg ttc ttc aac tgg aag cag gaa ttc agg act ctg      2021
Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln Glu Phe Arg Thr Leu
            650                 655                 660
```

Fig. 1C

```
gag gtc aca ctc cgg gat ttc agc aag ttg aat aag caa gat atc aca        2069
Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn Lys Gln Asp Ile Thr
        665                     670             675

tat ctg ggg aaa ata ttc agc tct gcc aca agc ctc agg ctg caa ata        2117
Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser Leu Arg Leu Gln Ile
        680                     685             690

aag aga tgt gct ggt gtg gct gga agc ctc agt ttg gtc ctc agc acc        2165
Lys Arg Cys Ala Gly Val Ala Gly Ser Leu Ser Leu Val Leu Ser Thr
695                     700             705                 710

tgt aag aac att tat tct ctc atg gtg gaa gcc agt ccc ctc acc ata        2213
Cys Lys Asn Ile Tyr Ser Leu Met Val Glu Ala Ser Pro Leu Thr Ile
                715             720                 725

gaa gat gag agg cac atc aca tct gta aca aac ctg aaa acc ttg agt        2261
Glu Asp Glu Arg His Ile Thr Ser Val Thr Asn Leu Lys Thr Leu Ser
                730             735                 740

att cat gac cta cag aat caa cgg ctg ccg ggt ggt ctg act gac agc        2309
Ile His Asp Leu Gln Asn Gln Arg Leu Pro Gly Gly Leu Thr Asp Ser
                745             750                 755

ttg ggt aac ttg aag aac ctt aca aag ctc ata atg gat aac ata aag        2357
Leu Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys
        760             765                 770

atg aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg        2405
Met Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu
775                 780                 785                 790

aag aag atg tgt tta ttt cat ttg acc cac ttg tct gac att gga gag        2453
Lys Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu
                795             800                 805

gga atg gat tac ata gtc aag tct ctg tca agt gaa ccc tgt gac ctt        2501
Gly Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu
                810             815                 820

gaa gaa att caa tta gtc tcc tgc tgc ttg tct gca aat gca gtg aaa        2549
Glu Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys
        825             830                 835

atc cta gct cag aat ctt cac aat ttg gtc aaa ctg agc att ctt gat        2597
Ile Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp
        840             845                 850

tta tca gaa aat tac ctg gaa aaa gat gga aat gaa gct ctt cat gaa        2645
Leu Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu
855                 860                 865                 870

ctg atc gac agg atg aac gtg cta gaa cag ctc acc gca ctg atg ctg        2693
Leu Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu
                875             880                 885
```

Fig. 1D

```
ccc tgg ggc tgt gac gtg caa ggc agc ctg agc agc ctg ttg aaa cat       2741
Pro Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His
            890                 895                 900

ttg gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa aac tgg aga       2789
Leu Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg
        905                 910                 915

ctc aca gat aca gag att aga att tta ggt gca ttt ttt gga aag aac       2837
Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn
        920                 925                 930

cct ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc       2885
Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser
935                 940                 945                 950

agt gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag caa       2933
Ser Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln
                955                 960                 965

tta gtg ttt ttt gac ttt agt act aaa gaa ttt cta cct gat cca gca       2981
Leu Val Phe Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro Asp Pro Ala
                970                 975                 980

tta gtc aga aaa ctt agc caa gtg tta tcc aag tta act ttt ctg caa       3029
Leu Val Arg Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln
            985                 990                 995

gaa gct agg ctt gtt ggg tgg caa ttt gat gat gat gat ctc agt gtt       3077
Glu Ala Arg Leu Val Gly Trp Gln Phe Asp Asp Asp Asp Leu Ser Val
        1000                1005                1010

att aca ggt gct ttt aaa cta gta act gct taa ataaagtgta ctcgaagcca    3130
Ile Thr Gly Ala Phe Lys Leu Val Thr Ala  *
1015                1020

gta                                                                   3133
```

Fig. 1E

```
  1 ATGCTGAACGCTGGTCCCCTGGGCTCCCTTATTTCTTTCTCTATACTTTGTCTCTGTGTCTTTTTCTTTT
    TACGACTTGCGACCAGGGGACCCGAGGGAATAAAGAAAGAGATATGAAACAGAGACACAGAAAAAGAAAA
  1▷ M  L  N  A  G  P  L  G  S  L  I  S  F  S  I  L  C  L  C  V  F  F  F

 71 CCAAGTCTCTCGTTCCACCTAACGAGAAACACCCACAGAACAAGAAGGTATCTGGTCTACAAGAACTCGA
    GGTTCAGAGAGCAAGGTGGATTGCTCTTTGTGGGTGTCTTGTTCTTCCATAGACCAGATGTTCTTGAGCT
 24▷ S  K  S  L  V  P  P  N  E  K  H  P  Q  N  K  K  V  S  G  L  Q  E  L  E

141 GGCCTCACTGAAACGGAAAGCAAATACAAAGAAACTTTATTTTAAAAACATGTCTTGGTCTCCCAAGAAG
    CCGGAGTGACTTTGCCTTTCGTTTATGTTTCTTTGAAATAAAATTTTTGTACAGAACCAGAGGGTTCTTC
 47▷ A  S  L  K  R  K  A  N  T  K  K  L  Y  F  K  N  M  S  W  S  P  K  K

211 AGGGCAATTGGATTGCTCAGCCAGAGACCCTTGCAGGCAGACACACAAGCGGCTGGACGTCGAGAGGAAC
    TCCCGTTAACCTAACGAGTCGGTCTCTGGGAACGTCCGTCTGTGTGTTCGCCGACCTGCAGCTCTCCTTG
 71▷ R  A  I  G  L  L  S  Q  R  P  L  Q  A  D  T  Q  A  A  G  R  R  E  E

281 ACATCGGCGGAAGAACATACAAGCAGCTGGACGTCCAGAGGACGTTGAAGGGAGAATGCTGGCGGAAGAG
    TGTAGCCGCCTTCTTGTATGTTCGTCGACCTGCAGGTCTCCTGCAACTTCCCTCTTACGACCGCCTTCTC
 94▷ H  I  G  G  R  T  Y  K  Q  L  D  V  Q  R  T  L  K  G  E  C  W  R  K  S

351 CACACAACAGACATCGGCACGCCAGCAGGCCATCCACCAGAGGAACGACTCGGAGTTTGGCCTGGAGGTG
    GTGTGTTGTCTGTAGCCGTGCGGTCGTCCGGTAGGTGGTCTCCTTGCTGAGCCTCAAACCGGACCTCCAC
117▷ T  Q  Q  T  S  A  R  Q  Q  A  I  H  Q  R  N  D  S  E  F  G  L (E  V

421 AATTTCATAAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTTATAAAGCAAATCACAG
    TTAAAGTATTTCCTGTTATCGGCTCGGGAATAAGTTTCTTACCCTTACTGACAATATTTCGTTTAGTGTC
141▷ N  F  I  K  D  N  S  R  A  L  I  Q  R  M  G  M  T  V  I  K  Q  I  T

491 ATGACCTATTTGTATGGAATGTTCTGAATCGCGAAGAAGTAAACATCATTTGCTGCGAGAAGGTGGAGCA
    TACTGGATAAACATACCTTACAAGACTTAGCGCTTCTTCATTTGTAGTAAACGACGCTCTTCCACCTCGT
164▷ D  D  L  F  V  W  N  V  L  N  R  E  E  V  N  I  I  C  C  E  K  V  E  Q

561 GGATGCTGCTAGAGGGATCATTCACATGATTTTGAAAAAGGGTTCAGAGTCCTGTAACCTCTTTCTTAAA
    CCTACGACGATCTCCCTAGTAAGTGTACTAAAACTTTTTCCCAAGTCTCAGGACATTGGAGAAAGAATTT
187▷ D  A  A  R  G  I  I  H  M  I  L  K  K  G  S  E  S  C  N  L  F  L  K

631 TCCCTTAAGGAGTGGAACTATCCTCTATTTCAGGACTTGAATGGACAAAGTTTTGAGGAGACACAGAATT
    AGGGAATTCCTCACCTTGATAGGAGATAAAGTCCTGAACTTACCTGTTTCAAAACTCCTCTGTGTCTTAA
211▷ S  L  K  E  W  N  Y  P  L  F  Q  D  L  N  G  Q  S )F  E  E  T  Q  N

701 GGGTCTTCTTTAACATCACCTCTTCTCTAATAGGTCTTTTTCATCAGACATCAGAAGGAGACTTGGACGA
    CCCAGAAGAAATTGTAGTGGAGAAGAGATTATCCAGAAAAAGTAGTCTGTAGTCTTCCTCTGAACCTGCT
234▷W  V  F  F  N  I  T  S  S  L  I  G  L  F  H  Q  T  S  E  G  D  L  D  D

771 TTTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTTATCCCCTTGGTGAAGAT
    AAACCGAGTCCTAAATTTCCTGAACATGGTATGGGGTAGAAAAGACTTGAAAATAGGGGAACCACTTCTA
257▷ L  A  Q  D  L  K  D  L  Y  H  T  P  S  F  L  N  F  Y  P  L  G  E  D
```

Fig. 2A

841 ATTGACATTATTTTTTAACTTGAAAAGCACCTTCACAGAACCTGTCCTGTGGAGGAAGGACCAACACCATC
    TAACTGTAATAAAAATTGAACTTTTCGTGGAAGTGTCTTGGACAGGACACCTCCTTCCTGGTTGTGGTAG
281▷ I D I I F N L K S T F T E P V L W R K D Q H H

911 ACCGCGTGGAGCAGCTGACCCTGAATGGCCTCCTGCAGGCTCTTCAGAGCCCCTGCATCATTGAAGGGGA
    TGGCGCACCTCGTCGACTGGGACTTACCGGAGGACGTCCGAGAAGTCTCGGGGACGTAGTAACTTCCCCT
304▷ H R V E Q L T L N G L L Q A L Q S P C I I E G E

·981 ATCTGGCAAAGGCAAGTCCACTCTGCTGCAGCGAATTGCCATGCTCTGGGGCTCCGGAAAGTGCAAGGCT
     TAGACCGTTTCCGTTCAGGTGAGACGACGTCGCTTAACGGTACGAGACCCCGAGGCCTTTCACGTTCCGA
327▷ S G K G K S T L L Q R I A M L W G S G K C K A

1051 CTGACCAAGTTCAAAATTCGTCTTCTTCCTCCGTCTCAGCAGGGCCCAGGGTGGACTTTTTGAAACCCTCT
     GACTGGTTCAAGTTTAAGCAGAAGAAGGAGGCAGAGTCGTCCCGGGTCCCACCTGAAAAACTTTGGGAGA
351▷ L T K F K F V F F L R L S R A Q G G L F E T L

1121 GTGATCAACTCCTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGCG
     CACTAGTTGAGGACCTATATGGACCGTGTTAGTCCTTCGTCTGTAAGTACCGGTACGACGACTTCGACGC
374▷ C D Q L L D I P G T I R K Q T F M A M L L K L R

1191 GCAGAGGGTTCTTTTCCTTCTTGATGGCTACAATGAATTCAAGCCCCAGAACTGCCCAGAAATCGAAGCC
     CGTCTCCCAAGAAAAGGAAGAACTACCGATGTTACTTAAGTTCGGGGTCTTGACGGGTCTTTAGCTTCGG
397▷ Q R V L F L L D G Y N E F K P Q N C P E I E A

1261 CTGATAAAGGAAAACCACCGCTTCAAGAACATGGTCATCGTCACCACTACCACTGAGTGCCTGAGGCACA
     GACTATTTCCTTTTGGTGGCGAAGTTCTTGTACCAGTAGCAGTGGTGATGGTGACTCACGGACTCCGTGT
421▷ L I K E N H R F K N M V I V T T T T E C L R H

1331 TACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATATGACAGAAGACAGCGCCCAGGCTCTCATCCG
     ATGCCGTCAAACCACGGGACTGACGACTCCACCCCCTATACTGTCTTCTGTCGCGGGTCCGAGAGTAGGC
444▷ I R Q F G A L T A E V G D M T E D S A Q A L I R

1401 AGAAGTGCTGATCAAGGAGCTTGCTGAAGGCTTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAAT
     TCTTCACGACTAGTTCCTCGAACGACTTCCGAACAACGAGGTTTAAGTCTTTAGGTCCACGAACTCCTTA
467▷ E V L I K E L A E G L L L Q I Q K S R C L R N

1471 CTCATGAAGACCCCTCTCTTTGTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTC
     GAGTACTTCTGGGGAGAGAAACACCAGTAGTGAACACGTTAGGTCTACCCACTTTCACTCAAGGTGAGAG
491▷ L M K T P L F V V I T C A I Q M G E S E F H S

1541 ACACACAAACAACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACACAAACATAAAGG
     TGTGTGTTTGTTGCGACAAGGTATGGAAGATACTAGACAACTATGTCTTTTTGTTTGTGTTTGTATTTCC
514▷ H T Q T T L F H T F Y D L L I Q K N K H K H K G

1611 TGTGGCTGCAAGTGACTTCATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTGTTCTCC
     ACACCGACGTTCACTGAAGTAAGCCTCGGACCTGGTGACACCTCTGGATCGAGACCTCCCACACAAGAGG
537▷ V A A S D F I R S L D H C G D L A L E G V F S

1681 CACAAGTTTGATTTCGAACTGCAGGATGTGTCCAGCGTGAATGAGGATGTCCTGCTGACAACTGGGCTCC
     GTGTTCAAACTAAAGCTTGACGTCCTACACAGGTCGCACTTACTCCTACAGGACGACTGTTGACCCGAGG
561▷ H K F D F E L Q D V S S V N E D V L L L T T G L

Fig.2B

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1751  TCTGTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATTCTTTCACAAGTCATTCCAGGAGTACAC
      AGACATTTATATGTCGAGTTTCCAAGTTCGGTTTCATATTTAAGAAAGTGTTCAGTAAGGTCCTCATGTG
  584▷  L  C  K  Y  T  A  Q  R  F  K  P  K  Y  K  F  F  H  K  S  F  Q  E  Y  T


1821  AGCAGGACGAAGACTCAGCAGTTTATTGACGTCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGGTTAC
      TCGTCCTGCTTCTGAGTCGTCAAATAACTGCAGAGTACTCGGTCTCCTCCACTGGTTCCCCTTACCAATG
  607▷  A  G  R  R  L  S  S  L  L  T  S  H  E  P  E  E  V  T  K  G  N  G  Y


1891  TTGCAGAAAATGGTTTCCATTTCGGACATTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGT
      AACGTCTTTTACCAAAGGTAAAGCCTGTAATGTAGGTGAATATCGTCGGACGAGGCCATGTGGACACCCA
  631▷  L  Q  K  M  V  S  I  S  D  I  T  S  T  Y  S  S  L  L  R  Y  T  C  G


1961  CATCTGTGGAAGCCACCAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGG
      GTAGACACCTTCGGTGGTCCCGACAATACTTCGTGGAGCGTCGTCACATAGTTGTGCCGACGGAAGAGCC
  654▷  S  S  V  E  A  T  R  A  V  M  K  H  L  A  A  V  Y  Q  H  G  C  L  L  G


2031  ACTTTCCATCGCCAAGAGGCCTCTCTGGAGACAGGAATCTTTGCAAAGTGTGAAAAACACCACTGAGCAA
      TGAAAGGTAGCGGTTCTCCGGAGAGACCTCTGTCCTTAGAAACGTTTCACACTTTTTGTGGTGACTCGTT
  677▷  L  S  I  A  K  R  P  L  W  R  Q  E  S  L  Q  S  V  K  N  T  T  E  Q


2101  GAAATTCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACAT
      CTTTAAGACTTTCGGTATTTGTAGTTAAGGAAACATCTCACACCGTAGGTAAATATAGTTCTCTCATGTA
  701▷  E  I  L  K  A  I  N  I  N  S  F  V  E  C  G  I  H  L  Y  Q  E  S  T


2171  CCAAATCAGCCCTGAGCCAAGAATTTGAAGCTTTCTTTCAAGGTAAAAGCTTATATATCAACTCAGGGAA
      GGTTTAGTCGGGACTCGGTTCTTAAACTTCGAAAGAAAGTTCCATTTTCGAATATATAGTTGAGTCCCTT
  724▷  S  K  S  A  L  S  Q  E  F  E  A  F  F  Q  G  K  S  L  Y  I  N  S  G  N


2241  CATCCCCGATTACTTATTTGACTTCTTTGAACATTTGCCCAATTGTGCAAGTGCCCTGGACTTCATTAAA
      GTAGGGGCTAATGAATAAACTGAAGAAACTTGTAAACGGGTTAACACGTTCACGGGACCTGAAGTAATTT
  747▷  I  P  D  Y  L  F  D  F  F  E  H  L  P  N  C  A  S  A  L  D  F  I  K


2311  CTGGACTTTTATGGGGGAGCTATGGCTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGAATCCACATGG
      GACCTGAAAATACCCCCTCGATACCGAAGTACCCTTTTCCGACGTCTTCTGTGTCCACCTTAGGTGTACC
  771▷  L  D  F  Y  G  G  A  M  A  S  W  E  K  A  A  E  D  T  G  G  I  H  M


2381  AAGAGGCCCCAGAAACCTACATTCCCAGCAGGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAG
      TTCTCCGGGGTCTTTGGATGTAAGGGTCGTCCCGACATAGAAACAAGAAGTTGACCTTCGTCCTTAAGTC
  794▷  E  E  A  P  E  T  Y  I  P  S  R  A  V  S  L  F  F  N  W  K  Q  E  F  R


2451  GACTCTGGAGGTCACACTCCGGGATTTCAGCAAGTTGAATAAGCAAGATATCAGATATCTGGGGAAAATA
      CTGAGACCTCCAGTGTGAGGCCCTAAAGTCGTTCAACTTATTCGTTCTATAGTCTATAGACCCCTTTTAT
  817▷  T  L  E  V  T  L  R  D  F  S  K  L  N  K  Q  D  I  R  Y  L  G  K  I


2521  TTCAGCTCTGCCACAAGCCTCAGGCTGCAAATAAAGAGATGTGCTGGTGTGGCTGGAAGCCTCAGTTTGG
      AAGTCGAGACGGTGTTCGGAGTCCGACGTTTATTTCTCTACACGACCACACCGACCTTCGGAGTCAAACC
  841▷  F  S  S  A  T  S  L  R  L  Q  I  K  R  C  A  G  V  A  G  S  L  S  L


2591  TCCTCAGCACCTGTAAGAACATTTATTCTCTCATGGTGGAAGCCAGTCCCCTCACCATAGAAGATGAGAG
      AGGAGTCGTGGACATTCTTGTAAATAAGAGAGTACCACCTTCGGTCAGGGGAGTGGTATCTTCTACTCTC
  864▷  V  L  S  T  C  K  N  I  Y  S  L  M  V  E  A  S  P  L  T  I  E  D  E  R
```

Fig. 2C

2661 GCACATCACATCTGTAACAAACCTGAAAACCTTGAGTATTCATGACCTACAGAATCAACGGCTGCCGGGT
     CGTGTAGTGTAGACATTGTTTGGACTTTTGGAACTCATAAGTACTGGATGTCTTAGTTGCCGACGGCCCA
 887▷ H I T S V T N L K T L S I H D L Q N Q R L P G

2731 GGTCTGACTGACAGCTTGGGTAACTTGAAGAACCTTACAAAGCTCATAATGGATAACATAAAGATGAATG
     CCAGACTGACTGTCGAACCCATTGAACTTCTTGGAATGTTTCGAGTATTACCTATTGTATTTCTACTTAC
 911▷ G L T D S L G N L K N L T K L I M D N I K M N

2801 AAGAAGATGCTATAAAACTAGCTGAAGGCCTGAAAAAACCTGAAGAAGATGTGTTTATTTCATTTGACCCA
     TTCTTCTACGATATTTTGATCGACTTCCGGACTTTTTGGACTTCTTCTACACAAATAAAGTAAACTGGGT
 934▷ E E D A I K L A E G L K N L K K M C L F H L T H

2871 CTTGTCTGACATTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCTGTGACCTTGAA
     GAACAGACTGTAACCTCTCCCTTACCTAATGTATCAGTTCAGAGACAGTTCACTTGGGACACTGGAACTT
 957▷ L S D I G E G M D Y I V K S L S S E P C D L E

2941 GAAATTCAATTAGTCTCCTGCTGCTTGTCTGCAAATGCAGTGAAAATCCTAGCTCAGAATCTTCACAATT
     CTTTAAGTTAATCAGAGGACGACGAACAGACGTTTACGTCACTTTTAGGATCGAGTCTTAGAAGTGTTAA
 981▷ E I Q L V S C C L S A N A V K I L A Q N L H N

3011 TGGTCAAACTGAGCATTCTTGATTTATCAGAAAATTACCTGGAAAAAGATGGAAATGAAGCTCTTCATGA
     ACCAGTTTGACTCGTAAGAACTAAATAGTCTTTTAATGGACCTTTTTCTACCTTTACTTCGAGAAGTACT
1004▷ L V K L S I L D L S E N Y L E K D G N E A L H E

3081 ACTGATCGACAGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAA
     TGACTAGCTGTCCTACTTGCACGATCTTGTCGAGTGGCGTGACTACGACGGGACCCCGACACTGCACGTT
1027▷ L I D R M N V L E Q L T A L M L P W G C D V Q

3151 GGCAGCCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTCCCACAACTCGTCAAGCTTGGGTTGAAAAACT
     CCGTCGGACTCGTCGGACAACTTTGTAAACCTCCTCCAGGGTGTTGAGCAGTTCGAACCCAACTTTTTGA
1051▷ G S L S S L L K H L E E V P Q L V K L G L K N

3221 GGAGACTCACAGATACAGAGATTAGAATTTTAGGTGCATTTTTTGGAAAGAACCCTCTGAAAAACTTCCA
     CCTCTGAGTGTCTATGTCTCTAATCTTAAAATCCACGTAAAAAACCTTTCTTGGGAGACTTTTTGAAGGT
1074▷ W R L T D T E I R I L G A F F G K N P L K N F Q

3291 GCAGTTGAATTTGGCGGGAAATCGTGTGAGCAGTGATGGATGGCTTGCCTTCATGGGTGTATTTGAGAAT
     CGTCAACTTAAACCGCCCTTTAGCACACTCGTCACTACCTACCGAACGGAAGTACCCACATAAACTCTTA
1097▷ Q L N L A G N R V S S D G W L A F M G V F E N

3361 CTTAAGCAATTAGTGTTTTTTTGACTTTAGTACTAAAGAATTTCTACCTGATCCAGCATTAGTCAGAAAAC
     GAATTCGTTAATCACAAAAAAACTGAAATCATGATTTCTTAAAGATGGACTAGGTCGTAATCAGTCTTTTG
1121▷ L K Q L V F F D F S T K E F L P D P A L V R K

3431 TTAGCCAAGTGTTATCCAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTTGGGTGGCAATTTGATGATGA
     AATCGGTTCACAATAGGTTCAATTGAAAAGACGTTCTTCGATCCGAACAACCCACCGTTAAACTACTACT
1144▷ L S Q V L S K L T F L Q E A R L V G W Q F D D D

3501 TGATCTCAGTGTTATTACAGATGAGAAAGCTCAGATGATTTGCCCATGGGTTATAAAAACTACTTCCTTAC
     ACTAGAGTCACAATAATGTCTACTCTTTCGAGTCTACTAAACGGGTACCCAATATTTTTGATGAAGGAATG
1167▷ D L S V I T D E K A Q M I C P W V I K L L P Y

Fig. 2D

3571 ACAGTGGCAGCATCAGAACTGGAATTCAGATCTCTTGCCTCCTAG
      TGTCACCGTCGTAGTCTTGACCTTAAGTCTAGAGAACGGAGGATC
1191▶ T V A A S E L E F R S L A S

Fig. 2E

Fig. 3
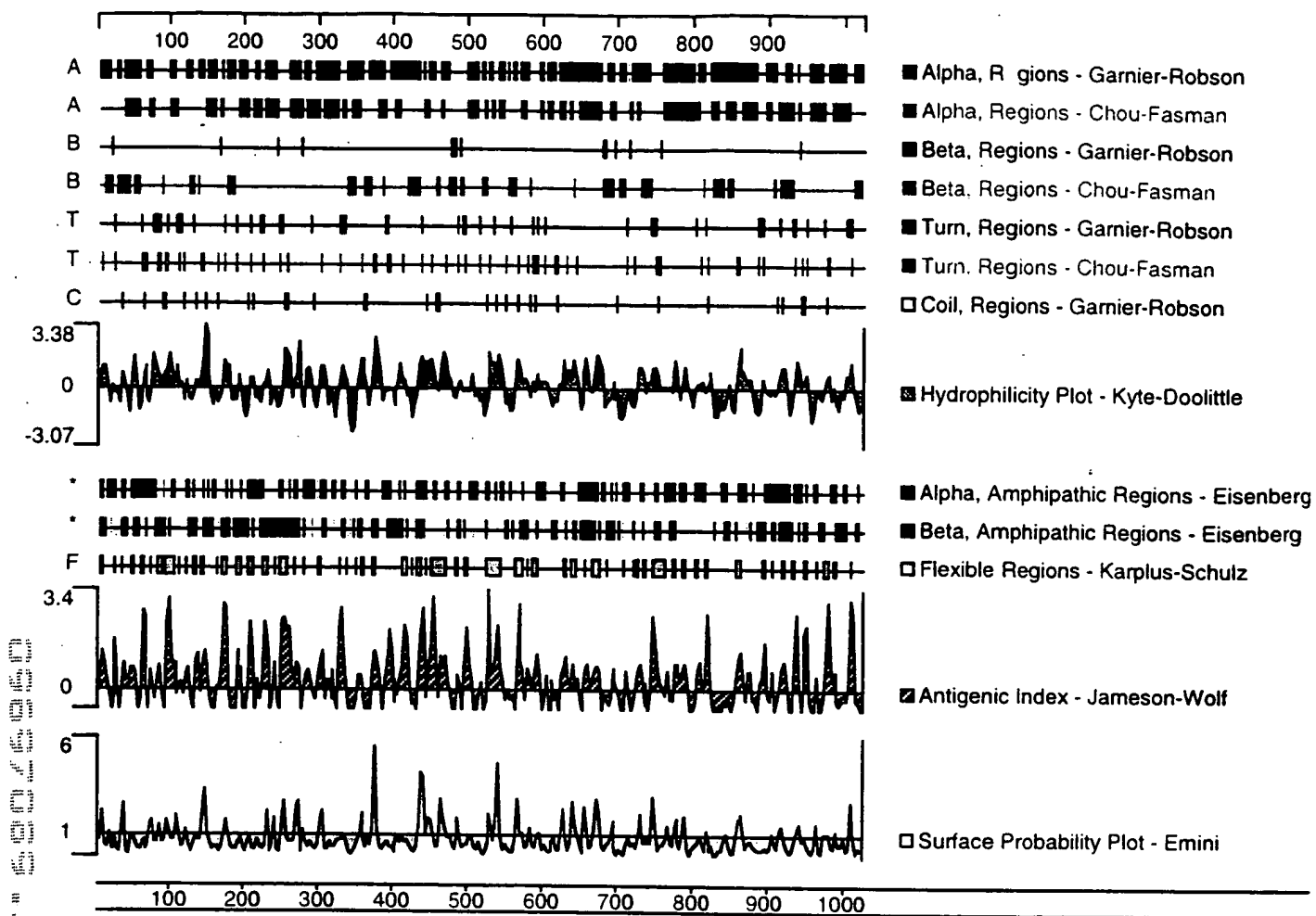
Fig. 4

```
CARD: domain 1 of 1, from 2 to 88: score 16.0, E = 0.0065
   SEQ ID NO: 7   *->aeddrrllrknrlellgeltlsglLdhLleknvLteeeeEkikaknt
                     + ++    ++ +   +g  +++++ d+L   nvL++ee+  i  +
      CARD12     2   --NFIKDNSRALIQRMGMTVIKQITDDLFVWNVLNREEVNIICCEKV 46

                  trrdkareLiDsvqkkGnqAfqiFlqaLretdqelladlllde<-*
                  ++ d ar  i +++kkG++ +++Fl +L+e ++ l +dl  +
      CARD12    47 EQ-DAARGIIHMILKKGSESCNLFLKSLKEWNYPLFQDLNGQS      88
```

$Fig. 5A$

```
LRR: domain 1 of 4, from 764 to 791: score 0.6, E = 8.2e+02
   SEQ ID NO: 8   *->nLeeLdLsnN.Lt.....slppglfsnLp<-*
                     nL++L ++n +  +++  +l +g ++nL+
      CARD12   764     NLTKLIMDNIkMNeedaiKLAEG-LKNLK      791
```

$Fig. 5B$

```
LRR: domain 2 of 4, from 821 to 848: score 0.3, E = 9.3e+02
   SEQ ID NO: 9   *->nLeeLdLsnN.Lt....slppglfsnLp<-*
                     Lee+ L ++ L+ + ++    ++nL
      CARD12   821     DLEEIQLVSCcLSanavKILAQNLHNLV      848
```

$Fig. 5C$

```
LRR: domain 3 of 4, from 849 to 872: score 11.2, E = 23
   SEQ ID NO: 8   *->nLeeLdLsnN.Ltslppglfsnlp<-*
                     +L  LdLs N L++  +++++ L
      CARD12   849     KLSILDLSENyLEKDGNEALHELI      872
```

$Fig. 5D$

```
LRR: domain 4 of 4, from 938 to 965: score 4.2, E = 2.5e+02
   SEQ ID NO: 8   *->nLeeLdLsnN.Lt.....slppglfsnLp<-*
                     n + L+L +N+ ++++   +   +f+nL+
      CARD12   938     NFQQLNLAGNrVSsdgwlAFMG-VFENLK      965
```

$Fig. 5E$

```
        E . L . . . . . . . L . S . . . . E G E . G . G K . . L L . . I A . L W . S G   Consensus #1
        E Q L V L N G V L G A L N S V C I V E G E A G S G K S V L L Q K I A F L W G S G   Majority
                    10                  20                  30                  40
   1    E Q L T L N G L L Q A L Q S P C I I E G E S G K G K S T L L Q R I A M L W G S G   CARD12-C
   1    E P L V L P E V F G N L N S V M C V E G E A G S G K T V L L K K I A F L W A S G   NAIP-C (SEQ ID NO:9)

        . C . L . . F . . V F . L . L S . . R . . . G L . . . . C D Q L L . . . G . .   Consensus #1
        K C K A L T K F Q L V F F L S L S S T R A D G G L A S I L C D Q L L D I E G S V   Majority
                    50                  60                  70                  80
   41   K C K A L T K F K F V F F L R L S - - R A Q G G L F E T L C D Q L L D I P G T I   CARD12-C
   41   C C P L L N R F Q L V F Y L S L S S T R P D E G L A S I I C D Q L L E K E G S V   NAIP-C

        . . . . . . . . . . . . . L . . . V L F L L D . Y . E . . . . . C . . . . . I . L   Consensus #1
        T E Q T F R A I L L Q L K N Q V L F L L D G Y N E I K P Q N C S I P Q V I G A L   Majority
                    90                  100                 110                 120
   79   R K Q T F M A M L L K L R Q R V L F L L D G Y N E F K P Q N C P E - - - I E A L   CARD12-C
   81   T E M C M R N I I Q Q L K N Q V L F L L D D Y K E I - - - - C S I P Q V I G K L   NAIP-C

        I . . N H . . . . . . . . . . . . . T . . . R . I R . . . . . . . . E . . . . . . . .   Consensus #1
        I Q E N H L S K T C V L V A V T T E R A R D I R Q F G A L I A E V G A F T E D S   Majority
                    130                 140                 150                 160
   116  I K E N H R F K N M V I V T T T T E C L R H I R Q F G A L T A E V G D M T E D S   CARD12-C
   117  I Q K N H L S R T C L L I A V R T N R A R D I R R Y L E T I L E I Q A F P F Y N   NAIP-C

        . . . . . . R . . . . . . . . . . . . . . . . . . . . . K . . . L . . . . K T P L F V .   Consensus #1
        A V A L L R E V L I K E L A E L R G L L V Q I G K S Q S L Q N L Q K T P L F V A   Majority
                    170                 180                 190                 200
   156  A Q A L I R E V L I K E L A E - - G L L L Q I Q K S R C L R N L M K T P L F V V   CARD12-C
   157  T V C I L R K L F S H N M T R L R K F M V Y F G K N Q S L Q K I Q K T P L F V A   NAIP-C

        . . C A . . . . . . . F . . . . . . . . . . . F . . . . . L . . . N K . . . . . .   Consensus #1
        A I C A I Q W G E S E F D S S F T D V A V F K S F Y D L L I L K N K H K H K G V   Majority
                    210                 220                 230                 240
   194  I T C A I Q M G E S E F H S H - T Q T T L F H T F Y D L L I Q K N K H K H K G V   CARD12-C
   197  A I C A - H W F Q Y P F D P S F D D V A V F K S Y M E R L S L R N K - - - - - -   NAIP-C

        A . . . . . . . . . . . C G . L A L . G . F S . . F . F . . . D . . . . . V . E   Consensus #1
        A A A D I L K A T V S S C G D L A L E G V F S H K F D F E L D D V A E A G V D E   Majority
                    250                 260                 270                 280
   233  A A S D F I R S - L D H C G D L A L E G V F S H K F D F E L Q D V S - - S V N E   CARD12-C
   230  A T A E I L K A T V S S C G E L A L K G F F S C C F E F N D D L A E A G V D E   NAIP-C

        D . . L T . . L . . K . T A Q R . . P . Y . F . . . . F Q E . . A G . R L . . L   Consensus #1
        D V L L T T G L L S K F T A Q R L K P K Y K F L S K A F Q E F L A G R R L I S L   Majority
                    290                 300                 310                 320
   270  D V L L T T G L L C K Y T A Q R F K P K Y K F F H K S F Q E Y T A G R R L S S L   CARD12-C
   270  D E D L T M C L M S K F T A Q R L R P F Y R F L S P A F Q E F L A G M R L I E L   NAIP-C
```

Fig. 6A

Alignment Report of Untitled, using Clu████method with PAM250 residue weight table.
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       L.S...E...G...L...S.....S.Y..L.Y......  Consensus #1
       LTSDEQEEVTLGLGHLQQIVSISDIVSAYSSLLNYVSGLS  Majority
              330         340         350         360

310    LTSHEPEEVTKGNGYLQKMVSISDITSTYSSLLRYTCG-S  CARD12-C
310    LDSDRQEHQDLGLYHLKQINSPMMTVSAYNNFLNYVSSLP  NAIP-C


       S..A......HL..........L...S....L..Q.....  Consensus #1
       SVEAGRAVVSHLAAVVDNKGSLLGLSIADDYLKHQESISL  Majority
              370         380         390         400

349    SVEATRAVMKHLAAVYQH-GCLLGLSIAKRPLWRQES---  CARD12-C
350    STKAGPKIVSHLLHLVDNKESLENISENDDYLKHQPEISL  NAIP-C


       ....L..........Q..............V.....YQ..T..  Consensus #1
       QMQLLQGVKNITEQAILSAVSINLLVLAGITAYQSSTVAA  Majority
              410         420         430         440

385    ----LQSVKNTTEQEILKAININSFVECGIHLYQESTSKS  CARD12-C
390    QMQLLRGLWQICPQAYFSMVSEHLLVLALKTAYQSNTVAA  NAIP-C


       ........F.QG..L.....N...Y...FF.H.P...S.L  Consensus #1
       ALSQVLEAFLQGKSLTLGAGNLPDYLFDFFDHLPESASAL  Majority
              450         460         470         480

421    ALSQEFEAFFQGKSLYINSGNIPDYLFDFFEHLPNCASAL  CARD12-C
430    CSPFVLQ-FLQGRTLTLGALNL-QY---FFDH-PESLSLL  NAIP-C


       ..I......G..................P.....Y...  Consensus #1
       DSIKLSIRGGATASRAKAAVLTGGIDKSEAPTIDETYIPA  Majority
              490         500         510         520

461    DFIKLDFYGGAMASWEKAAEDTGGIHMEEAP---ETYIPS  CARD12-C
464    RSIHFSIRGNKTSPRAHFSVLETCFDKSQVPTIDQDY--A  NAIP-C


       .A.....W.....E...............L.....  Consensus #1
       SAVSLFNEWEQELATLEVTVKSFSDLNKQAITDLGTGFSS  Majority
              530         540         550         560

498    RAVSLFFNWKQEFRTLEVTLRDFSKLNKQDITYLGKIFSS  CARD12-C
502    SAFEPMNEWERNLAEKEDNVKSYMDMQRRASPDLSTGYWK  NAIP-C


       .......I..C...............L.V......  Consensus #1
       ASSLQLQIKRCAGVAGSLSLVLSTCKNIYSLEVDASDLTV  Majority
              570         580         590         600

538    ATSLRLQIKRCAGVAGSLSLVLSTCKNIYSLMVEASPLTI  CARD12-C
542    LSPKQYKI-PC----------------------LEVDVNDIDV  NAIP-C


       ..............S.......QR....L..S.......  Consensus #1
       VGEDHLTIVTNLTVLSIHDLASQRLEGGLTDSLGNLKGLI  Majority
              610         620         630         640

578    EDERHITSVTNLKTLSIHDLQNQRLPGGLTDSLGNLKNLT  CARD12-C
562    VGQDMLEIL--MTVFS----ASQRIELHLNHS----RGFI  NAIP-C
```

Fig. 6B

Alignment Report of Untitled, using Cl████ method with PAM250 residue weight table.
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        . . I . . . . . . . . . . . . . K . . . . . . . . . . . . . C . . . . . . . L S . . . . .   Consensus #1
        E L I R D A L E L S E A S A I K L A E G L K N L K K M C L I S L L E L S A A G E   Majority
                        650             660             670             680

618  K L I M D N I K M N E E D A I K L A E G L K N L K K M C L F H L T H L S D I G E   CARD12-C
592  E S I R P A L E L S K A S V T K - - - - - - - - - - - C S I S K L E L S A A E Q   NAIP-C


        . . . . . . . . S L . S . . . . L E . . . . . . . . . . . . . . . . . . . Q . . . N   Consensus #1
        G L L L I V K S L S S E P C D L E E I Q L V S C C L V A G A V Q I L A Q I L H N   Majority
                        690             700             710             720

658  G M D Y I V K S L S S E P C D L E E I Q L V S C C L S A N A V K I L A Q N L H N   CARD12-C
621  E L L L T L P S L E S - - - - L E - - - - - - - - - - V S G T I Q S Q D Q I F P N   NAIP-C


        L . K . . . L . L . E . . . . . . G N . . . . . . I . . . . . . . . . . . . L .   Consensus #1
        L V K L S I L D L S E L S V D L D G N I A V H S V I P D E F N V L E Q L T A L L   Majority
                        730             740             750             760

698  L V K L S I L D L S E N Y L E K D G N E A L H E L I - D R M N V L E Q L T A L M   CARD12-C
648  L D K F - - L C L K E L S V D L E G N I N V F S V I P E E F P N F H H M E K L L   NAIP-C


        . . . . . . . . . . . S . L . . . L . . . . . L . . L . L . . . . . . D . E . .   Consensus #1
        L Q I G A D V D G S L S S L V A S L E E V I S L V I L G L E G Q Q L T D T E I S   Majority
                        770             780             790             800

737  L P W G C D V Q G S L S S L L K H L E E V P Q L V K L G L K N W R L T D T E I R   CARD12-C
686  I Q I S A E Y D P - - S K L V A S L P N F I S L K I L N L E G Q Q F P D E E T S   NAIP-C


        . . . A . . . . . . . L . N . . . L . L . . . . . . . . . . . . . G . . . . . . K   Consensus #1
        I L G A F I G L G S L S N L E E L I L A G G D V S S D G W L A F M G V F E V A K   Majority
                        810             820             830             840

777  I L G A F F G K N P L K N F Q Q L N L A G N R V S S D G W L A F M G V F E N L K   CARD12-C
724  E K F A Y I - L G S L S N L E E L I L P T G D - - - - - - - - - - G I Y R V A K   NAIP-C


        . . . . . . . . . . . . . . . . . . . . . L . . L . L . F . . . . . . . . .   Consensus #1
        L L V F F D F S T K E F L P D P A L V Q Q L S Q V L S V L S F L Q T A R L V G W   Majority
                        850             860             870             880

817  Q L V F F D F S T K E F L P D P A L V R K L S Q V L S K L T F L Q E A R L V G W   CARD12-C
753  L I I - - - - - - - - - - - - - - Q Q C Q Q L - H C L R V L S F F K T - - - - -   NAIP-C


        . . . D D . . . . . I . . . . . . . . . .   Consensus #1
        Q L D D D S V V V I T G A F K L V T G   Majority
                        890

857  Q F D D D D L S V I T G A F K L V T A   CARD12-C
773  - L N D D S V V E I - - - - - - - - G   NAIP-C
```

Consensus 'Consensus #1': When all match the residue of CARD12-C show the residue of CARD12-C, otherwise show '.'.

Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #1' exactly.

Fig. 6C